

p27^{Kip1}, a double-edged sword in Shh-mediated medulloblastoma

Tumor accelerator and suppressor

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Medulloblastoma, a brain tumor arising in the cerebellum, is the most common solid childhood malignancy. The current standard of care for medulloblastoma leaves survivors with life-long side effects. Gaining insight into mechanisms regulating transformation of medulloblastoma cells-of-origin may lead to development of better treatments for these tumors. Cerebellar granule neuron precursors (CGNPs) are proposed cells of origin for certain classes of medulloblastoma, specifically those marked by aberrant Sonic hedgehog (Shh) signaling pathway activation. CGNPs require signaling by Shh for proliferation during brain development. In mitogen-stimulated cells, nuclear localized cyclin-dependent kinase (Cdk) inhibitor p27^{Kip1} functions as a checkpoint control at the G₁- to S-phase transition by inhibiting Cdk2. Recent studies have suggested that cytoplasmically localized p27^{Kip1} acquires oncogenic functions. Here, we show that p27^{Kip1} is cytoplasmically localized in CGNPs and mouse Shh-mediated medulloblastomas. Transgenic mice bearing an activating mutation in the Shh pathway and lacking one or both p27^{Kip1} alleles have accelerated tumor incidence compared to mice bearing both p27^{Kip1} alleles. Interestingly, mice heterozygous for p27^{Kip1} have decreased survival latency compared to p27^{Kip1}-null animals. Our data indicate that this may reflect the requirement of at least one copy of p27^{Kip1} for recruiting cyclin D/Cdk4/6 to promote cell cycle progression, yet insufficient expression in the heterozygous or null state to inhibit cyclin E/Cdk2. Finally, we find that mislocalized p27^{Kip1} may play a positive role in motility in medulloblastoma cells. Together, our data indicate that the dosage of p27^{Kip1} plays a role in cell cycle progression and tumor suppression in Shh-mediated medulloblastoma expansion.

Introduction

Medulloblastoma is the most common solid tumor found in children. These tumors arise in young children in the cerebellum, a part of the brain that develops post-natally in children and mice.¹ Some types of medulloblastoma are proposed to arise from proliferating CGNPs that fail to exit the cell cycle, migrate and/or differentiate.² CGNP proliferation requires activation of the Shh pathway. Shh is secreted from Purkinje cells in the cerebellum and binds to its receptor Patched (Ptc) on CGNPs, which prevents inhibition of Smoothened (Smo) and activates transcription of Shh targets, such as the Gli transcription factors, N-myc and the D-type cyclins, to drive CGNP proliferation.³⁻⁵ Mutations causing aberrant activation of the Shh signaling pathway are implicated in human and mouse medulloblastomas.^{6,7} To promote proliferation and oncogenic transformation, Shh alone is not sufficient; cooperative interactions with other signaling pathways are required.^{4,8-12}

CGNP proliferation is regulated by cyclin dependent kinases (Cdk4/6) in cooperation with D-type cyclins.¹³⁻¹⁴ However, cell

cycle progression in cerebellar development is often controlled by Cdk inhibitors, p18^{INK4c} and p27^{Kip1}.¹⁵ While p18^{INK4c} preferentially targets Cdk4 and Cdk6, p27^{Kip1} has three distinct roles: (1) mediates cyclin D/Cdk4/6 assembly formation; (2) controls the late G1 phase by binding to and inhibiting Cdk2 and cyclin E; (3) regulates cell motility by binding to and inhibiting RhoA.¹⁶⁻²⁴ In the cerebellum, nuclear p27^{Kip1} is found in post-mitotic and differentiated CGNPs, suggesting its ability to regulate cell cycle exit.²⁵ Indeed, losing p27^{Kip1} in cerebellar development accelerates CGNP proliferation.^{15,25} Low levels of p27^{Kip1} have been linked with high-grade tumors, including brain tumors such as astrocytoma and glioblastoma multiforme.²⁶⁻³⁰ Previous studies have shown that mislocalized p27^{Kip1} is associated with aggressive tumors, suggesting an oncogenic role in this context.³¹⁻³⁴ We previously reported that p27^{Kip1} is mislocalized in Shh-mediated medulloblastoma, and this localization is Akt- and TSC2-dependent.^{11,35} More recently, Ayrault et al. observed that mice heterozygous for Patched and either heterozygous or nullizygous for p27^{Kip1} develop medulloblastoma and with high penetrance and accelerated rate.⁸ In addition, these tumors retain the progenitor cell marker Math-1, which

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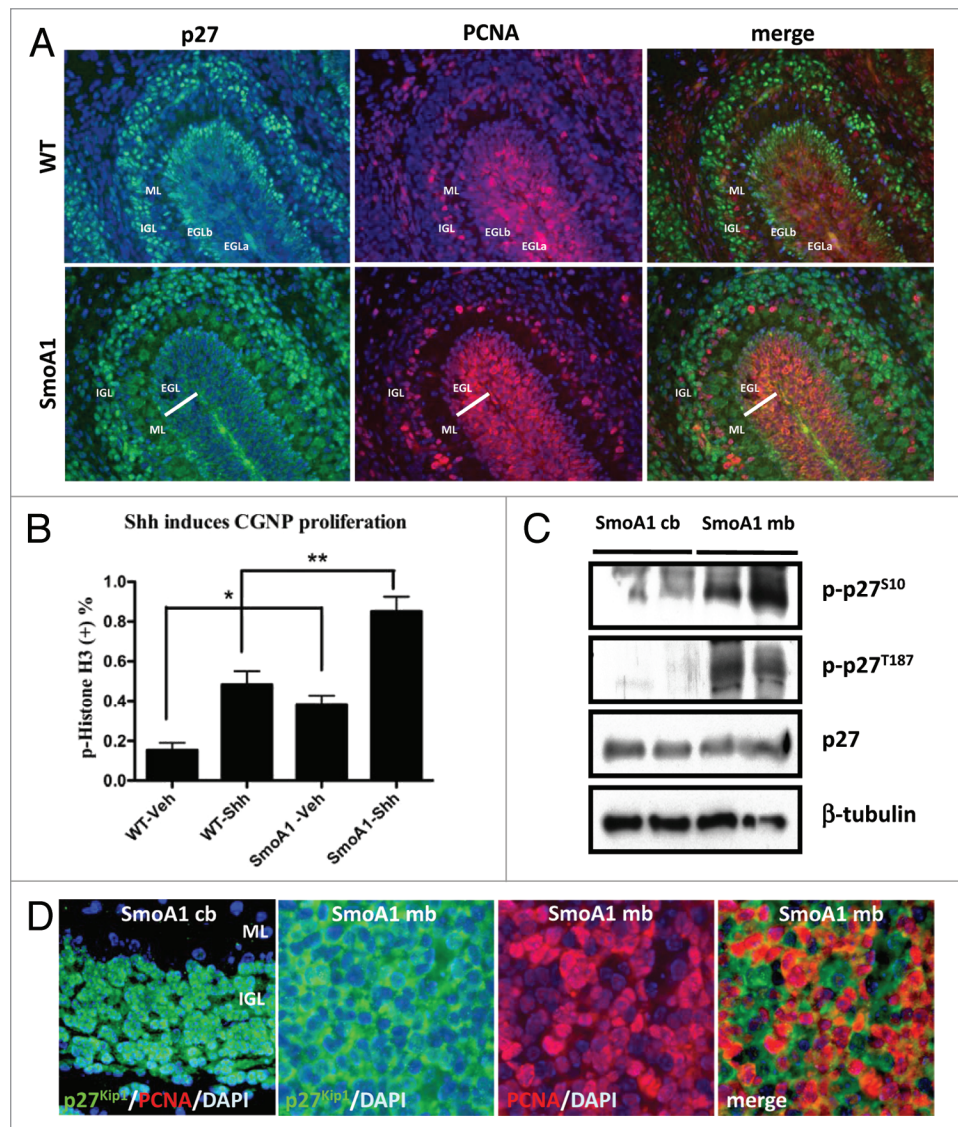


Figure 1. p27^{Kip1} is mislocalized in Shh-mediated medulloblastoma. (A) In cerebellar development of post-natal day 7, the peak for CGNP proliferation, p27^{Kip1} (green) is expressed in post-mitotic region, external granule layer b (EGLb), molecular layer (ML) and differentiated region inner granule layer (IGL), whereas aberrant Shh signaling leads to p27^{Kip1} mislocalization and increased CGNP proliferation throughout the EGL. Proliferation marker PCNA (red) stains CGNPs in proliferating region EGLa. (B) Wild-type and SmoA1 CGNPs were plated, treated with Shh and measured for proliferation by quantification of phospho-Histone H3. (C) While non-tumor cells undergo cell cycle exit and/or differentiation via p27^{Kip1} nuclear localization in the IGL, the Shh-induced medulloblastoma maintains misregulated phosphorylation of p27^{Kip1} at Ser10 and Thr187, which leads to mislocalization and inhibition of cell cycle regulation. (D) Non-tumors in NeuroD2-SmoA1 mice have nuclear p27^{Kip1} (first column), whereas SmoA1 medulloblastoma have cytoplasmic p27^{Kip1} (second column) and high proliferation (third and fourth column).

is expressed in proliferating CGNPs. These finding suggested that reduced levels of p27^{Kip1} could contribute to maintenance of a precursor cell phenotype that could be vulnerable to transforming events.

Here, using mice that express an activated mutant allele of the Shh receptor component Smoothed (SmoA1), we show that p27^{Kip1} is mislocalized in CGNPs and Shh-mediated medulloblastomas. We also find that SmoA1 mice lacking one or both p27^{Kip1} alleles have reduced survival compared to mice having two wild-type p27^{Kip1} alleles. Interestingly, SmoA1 mice heterozygous for p27^{Kip1} have decreased survival latency compared to mice lacking both copies of p27^{Kip1}. Our results suggest that this

may be due to retention of a single copy of p27^{Kip1} being sufficient to recruit cyclin D/Cdk4/6 to promote cell cycle progression yet insufficient to inhibit cyclin E/Cdk2. Finally, we show that p27^{Kip1} can interact with RhoA, perhaps contributing to tumor cell motility and invasion, and may underlie the more aggressive nature of p27^{Kip1} heterozygous medulloblastomas in comparison with the tumors arising in the p27^{Kip1}-null mice.

Results and Discussion

p27^{Kip1} is mislocalized in Shh-mediated medulloblastoma. We have previously observed that p27^{Kip1} is found in the cytoplasm

of medulloblastomas arising in NeuroD2-SmoA1 transgenic mice. These mice express an activated mutant allele of the Shh receptor component Smoothed in the cerebellar progenitor compartment.³⁶ Approximately 60% of these mice develop medulloblastoma by 6 months of age. To explore the contribution of nuclear and cytoplasmic p27^{Kip1} to Shh-driven CGNP proliferation and medulloblastoma, we analyzed cerebella in wild-type and SmoA1 mice at post-natal day 7, the peak of CGNP proliferation. In wild-type mice, p27^{Kip1} is present in the nucleus of CGNPs in the post-mitotic region of the external granule layer (EGLb) and in the differentiated region inner granule layer (IGL) (Fig. 1A). In contrast, SmoA1 mice have cytoplasmic p27^{Kip1} throughout the EGL, and this correlates with increased proliferation as determined by staining for Proliferating Cell Nuclear Antigen (PCNA, Fig. 1A).

Next, to confirm whether aberrant Shh signaling leads to increased CGNP proliferation, we cultured CGNPs from wild type and SmoA1 mice in the presence or absence of exogenous Shh. We found that vehicle-treated SmoA1 CGNPs have more phospho-Histone H3 (+) cells than wild-type cells (Fig. 1B). Addition of Shh to the growth medium increased proliferation of wild-type and SmoA1 CGNPs, with SmoA1 CGNPs proliferating at a significantly higher rate, suggesting that these mutant CGNPs are Shh-responsive and potentially benefit from cytoplasmic p27^{Kip1}.

Tumor cells benefit by phosphorylation and/or mislocalization of tumor suppressor genes.^{34,37-40} To determine whether this is the case for p27^{Kip1} in Shh-driven medulloblastomas, we utilized whole cell lysates from SmoA1 medulloblastoma tumors and adjacent cerebella. Using western blot analysis, we found that p27^{Kip1} is phosphorylated at Ser10, which is responsible for its nuclear export,⁴¹⁻⁴⁴ and at Thr187, which is regulated by active cyclin E and cyclin A/Cdk2 leading to Skp2-mediated ubiquitinated degradation (Fig. 1C).^{45,46} Using immunofluorescence analysis, as shown in Figure 1D, adult mouse cerebellar tissue features nuclear p27^{Kip1} in differentiated granule neurons occupying the internal granule layer (IGL). However, in SmoA1 medulloblastoma tissue, which is highly proliferative, p27^{Kip1} is found in the cytoplasm. Together, this suggests that misregulated Shh signaling alters p27^{Kip1} localization and is correlated with increased cell proliferation.

p27^{Kip1} gene dose affects medulloblastoma incidence and onset in SmoA1 mice. The transmembrane protein Patched (Ptc) is a tumor suppressor that negatively regulates Smoothed activity and whose loss is associated with medulloblastoma formation

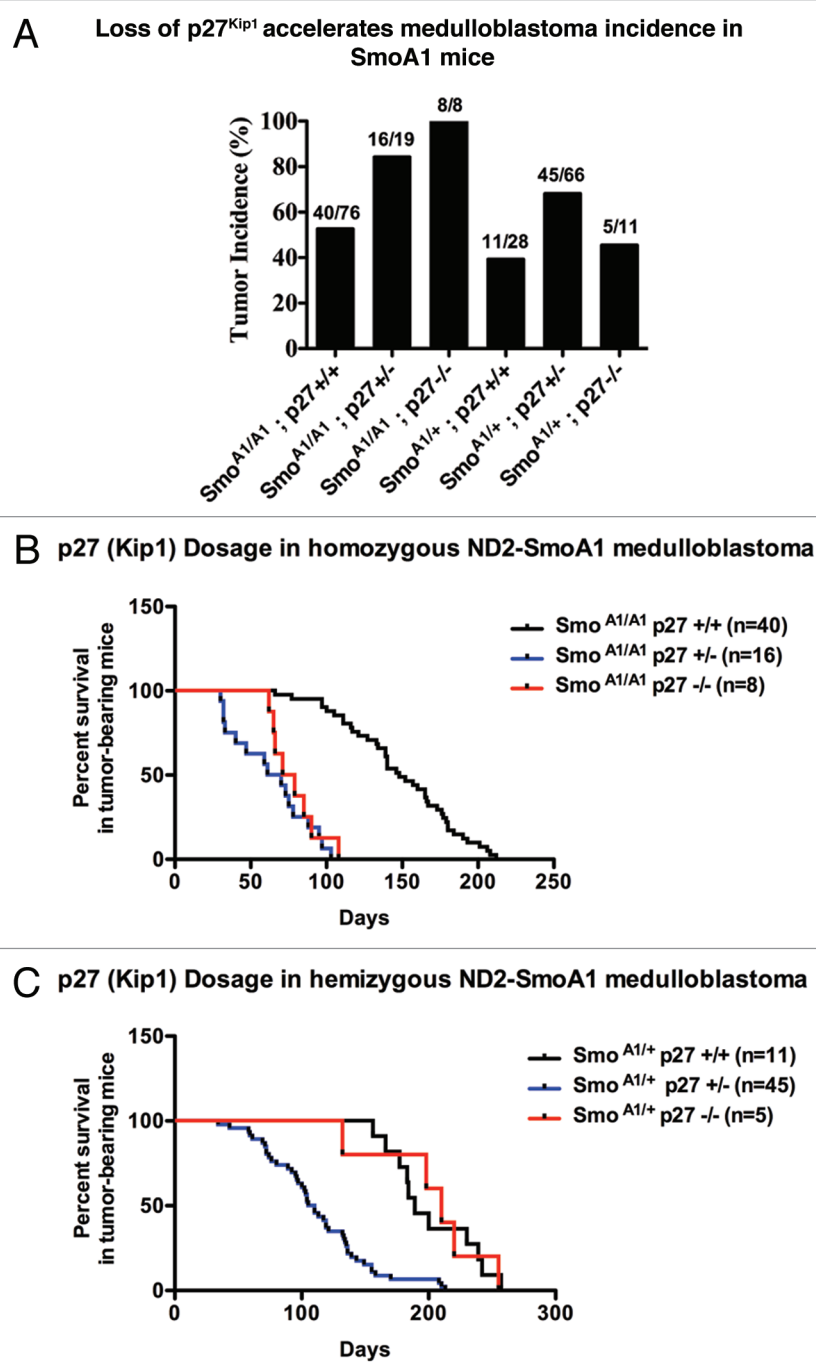


Figure 2 (A–C). p27^{Kip1} loss accelerates medulloblastoma incidence in SmoA1 mice. (A) p27^{Kip1} loss accelerates medulloblastoma incidence in homozygous and hemizygous mice for SmoA1 transgene. (B and C) SmoA1 mice heterozygous for p27^{Kip1} have a dramatic decreased survival latency compared to homozygous and nullizygous for p27^{Kip1}.

in humans.^{47,48} Similarly, mice heterozygous for Ptc are predisposed to develop medulloblastomas.⁴⁹ Recently, it has been reported that p27^{Kip1} hetero- or nullizygosity increases medulloblastoma incidence in Ptc^{+/-} mice.⁸ Activating mutations in Smoothed are also found in human medulloblastomas,⁵⁰ and this can be phenocopied in mice using the NeuroD2-SmoA1 and SmoM1/M2 alleles.^{36,51-52} To assess whether p27^{Kip1} gene dosage

and localization affects medulloblastoma formation in this model of constitutive Shh pathway activation, we generated homozygous *SmoA1* mice lacking one or both *p27^{Kip1}* alleles. *SmoA1* mice were previously reported to develop medulloblastoma at a high incidence (~90%) and a mean time of occurrence of 5 to 6 months.⁵³ We observed a lower medulloblastoma incidence (~53%) in our mouse colony (Fig. 2A). However, losing one or both *p27^{Kip1}* alleles increased tumor incidence to ~84% and ~100%, respectively. Among the homozygous *SmoA1* medulloblastoma-bearing mice, the *p27^{Kip1}* heterozygous mice have a reduced survival time (median survival of 61 days) than wild type (median survival of 147 days) and nullizygous (median survival of 71 days) (Fig. 2B).

Surprisingly, when we generated hemizygous *SmoA1* mice lacking one or both *p27* alleles, we observed that hemizygous *SmoA1* mice heterozygous for *p27^{Kip1}* have a higher tumor incidence (~68%) than wild type (~39%) or nullizygous for *p27^{Kip1}* (~45%). Among the hemizygous *SmoA1* medulloblastoma-bearing mice, the *p27^{Kip1}* heterozygous mice have a strikingly reduced survival time (median survival of 105 days) compared with wild-type (median survival of 186 days) and *p27* nullizygous mice (median survival of 204 days) (Fig. 2C). The increased tumor incidence and dramatically reduced survival of homozygous and hemizygous *SmoA1* medulloblastoma-bearing mice suggests *p27^{Kip1}* is haploinsufficient in Shh-mediated medulloblastomas. These results are consistent with reduced *p27^{Kip1}* function promoting enhanced CGNP transformation in the setting of activated Shh signaling.

To determine how *p27^{Kip1}* loss contributes to *SmoA1* medulloblastoma formation, we investigated how G1- and S-phase cell cycle regulators are affected by *p27^{Kip1}* reduction or loss in adult cerebella and medulloblastoma of *SmoA1* mice. We observed high protein levels of D-type cyclins in tumors compared to non-tumors (Fig. 2D). These tumors also maintained high levels of N-myc, a Shh transcriptional target;^{4,54} Bmi-1, a progenitor cell marker implicated in Shh-driven medulloblastoma;^{11,55-56} cyclin A and cyclin E. Consistent with our previous report, active mTOR signaling, which is vital for cell growth, was found in these tumors, based on ribosomal protein-S6 phosphorylation.¹¹ Finally, previous reports have shown that tyrosine phosphorylation of *p27^{Kip1}* by c-Abl and Src family kinases initiates the transition of *p27^{Kip1}* from inhibitor of cyclin E/Cdk2 in G0 phase to substrate of cyclin/Cdk2 in G1 phase, therefore making *p27^{Kip1}* a poor Cdk2 inhibitor and potentially a promoter of cyclin D/Cdk4 assembly.^{20,57-58} While we find Src to be present in both non-tumor tissue and tumors, we observed high levels of c-Abl in Shh-medulloblastoma. Thus, all of the tumors are highly proliferative, regardless of *p27* gene status.

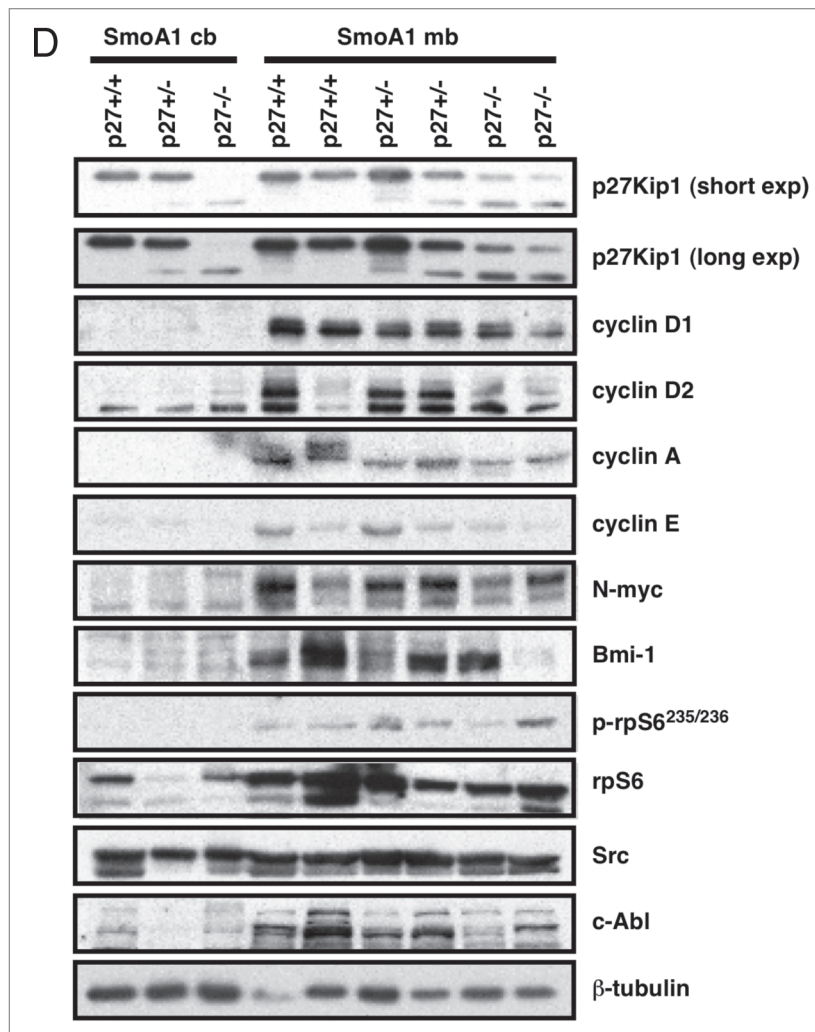


Figure 2D. *p27^{Kip1}* loss accelerates medulloblastoma incidence in *SmoA1* mice. (D) Western blot analysis of cell cycle indicators in NeuroD2-*SmoA1* medulloblastomas arising in wild-type, *p27^{+/-}* and *p27^{-/-}* mice.

Cyclin D/Cdk4/6 assembly is dependent on *p27^{Kip1}*. Progression from G1 to S phase of the cell cycle requires assembly of D-type cyclin:Cdk complexes.¹⁹ It has been shown that *p27^{Kip1}* has an essential role in assembly and stability of cyclin D/Cdk4/6 complexes.²⁰⁻²¹ We speculated that the increased aggressiveness of *p27^{Kip1}* heterozygous medulloblastomas in the hemizygous mice might be due to differential assembly of D-type cyclin:Cdk complexes in comparison to the *p27^{Kip1}*-null mice. Using co-immunoprecipitation and western blotting from cerebella and medulloblastomas from *SmoA1* mice, we found that *p27^{Kip1}* is bound with cyclin D1, Cdk4 and Cdk6 in tumors but not in the normal cerebella tissue (Fig. 3A). Next, to see if this assembly is affected by *p27^{Kip1}* gene dosage, we performed immunoprecipitation using tumors and cerebellar tissue from hemizygous *SmoA1* mice that are either wild type, heterozygous or nullizygous for *p27^{Kip1}*. We chose hemizygous *SmoA1* mice because of the significant effect *p27* heterozygosity has on tumor latency in that genetic background. We observed decreased interaction between cyclin D1 and Cdk6 as tumors lose *p27^{Kip1}* (Fig. 3B), which would

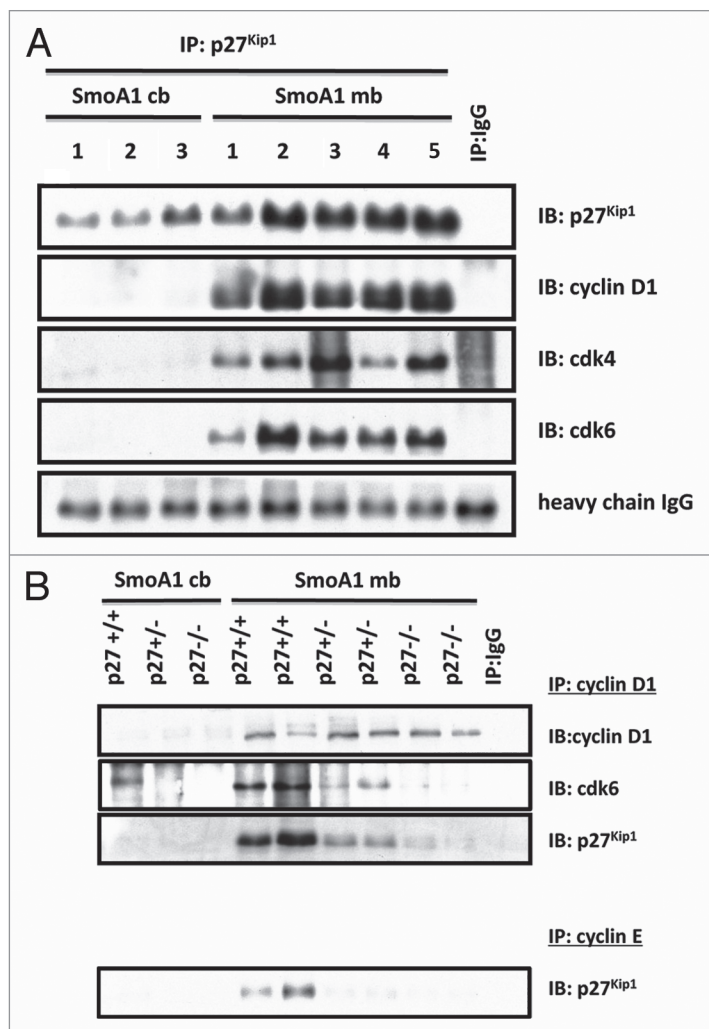


Figure 3. Cyclin D/Cdk4/6 assembly is dependent on p27^{Kip1}. (A) Immunoprecipitation shows p27^{Kip1} interacts with cyclin D1, Cdk4/6 in SmoA1 medulloblastoma. (B) Immunoprecipitation shows decreased cyclin D1/Cdk6 interaction as a result of p27^{Kip1} loss. Tumor proliferation benefits as cyclin E/p27^{Kip1} is decreased, suggesting p27^{Kip1} is haploinsufficient as a tumor suppressor.

be consistent with impaired cyclin D1:Cdk6 complex assembly, which may impede G1 cell cycle progression. In its role as a tumor suppressor and negative cell cycle regulator, p27^{Kip1} binds to and inhibits cyclin E/Cdk2 to prevent late G1-to-S progression, leading to cell cycle exit.¹⁹ Medulloblastomas that are heterozygous or null for p27^{Kip1} show less cyclin E bound to p27^{Kip1}, suggesting ongoing activity of the cyclin E:Cdk2 complex, which promotes pRb inactivation. Together, this may reflect the requirement for p27^{Kip1} in recruiting cyclin D/Cdk4/6 to promote cell cycle progression, yet insufficient to inhibit cyclin E/Cdk2 in these tumors.

Cytosolic p27^{Kip1} plays a role in cell motility in SmoA1 medulloblastoma. The observation that p27^{Kip1} is predominantly mislocalized rather than undergoing degradation in SmoA1 medulloblastomas suggests it may have a functional role in the cytoplasm of these tumor cells. Recent studies have suggested that cytoplasmic p27^{Kip1} plays an oncogenic role in mediating cell motility by preventing activation of RhoA, a regulator

of actin cytoskeleton in the formation of stress fibers (Fig. 4A).^{17,22,37,59-61} Cell migration is controlled by RhoA signaling and is dependent on RhoA to convert from the GDP-inactive state to GTP-active state.⁶² RhoA-GTP stabilizes actin stress fibers through the activation of its substrate Rho-associated, coiled-coil containing protein kinase (ROCK), which then phosphorylates and activates LIM domain-containing protein kinases (LIMK). LIMK in turn phosphorylates and inhibits the actin depolymerization-promoting protein cofilin, resulting in stabilization of stress fibers. See et al. showed that p27^{Kip1} deficiency in PDGF-expressing glial cells correlated with elevated levels of Rho-GTP and reduced cell migration.⁶³ We therefore asked whether p27^{Kip1} might play a role in cell motility in Shh-mediated medulloblastomas. We first co-stained p27^{Kip1} with phospho-LIMK and phospho-cofilin in these tumors and found an inverse relationship between p27^{Kip1} and these markers of motility inhibition, therefore suggesting that these tumor cells carrying cytoplasmic p27^{Kip1} have increased cell motility (Fig. 4B).

p27^{Kip1} can regulate cell migration by binding to RhoA, potentially interfering its GDP state-to-GTP state conversion and/or its relationship to activate ROCK.^{17,64-65} To determine a potential relationship between p27^{Kip1} and RhoA, we then carried out subcellular fractionation and immunoprecipitation/western blotting of these tumor cells and found that these proteins interact in the cytoplasm (Fig. 4C, 4D). Though p27^{Kip1} serves as a tumor suppressor to regulate cell cycle progression in the nucleus, it may also be stabilized in the cytoplasm to contribute to oncogenesis independent of its cell cycle functions to promote cell motility and invasion. Other members of the Cip/Kip class possess similar characteristics. Cytoplasmic p21^{Cip1} can inhibit ROCK activity, whereas p57^{Kip2} inhibits the function of LIMK by sequestering it in the cytoplasm, away from its substrate cofilin.^{23,38-39,66-67} We have previously shown the expression analysis of CDKN1B (p27^{Kip1}) in human Shh-subgroup medulloblastomas and found a moderate decrease compared with adult cerebellum.¹¹ p27^{Kip1} is not a classic tumor suppressor, as it is rarely mutated or deleted in cancer, but rather often deregulated in cancer by post-translational modifications.⁶⁸⁻⁶⁹ While our data suggest that p27^{Kip1} may be a useful biomarker, it is unknown whether cytoplasmic p27 is seen in human medulloblastoma. Therefore, more work is needed in human medulloblastoma studies to define its regulation, as it serves an important role in controlling tumor cell growth and could potentially serve as a therapeutic target in clinical trials.

Materials and Methods

Mice. Harvest of neural precursors from neonatal mice and preparation of cerebella and tumor tissue from wild-type and mutant mice for histological analysis were carried out in compliance with the Memorial Sloan-Kettering Institutional animal care and use committee guidelines. C57-BL6 wild-type mice (Jackson Laboratories), heterozygous and nullizygous p27 mice (kindly given by Andrew Koff of Memorial

Sloan-Kettering Cancer Center)⁷⁰ and *NeuroD2-SmoA1* mice (kindly provided by Jim Olson of Fred Hutchinson Cancer Research Center)³⁶ were used.

Genotyping. p27^{Kip1}-null male mice were bred to SmoA1 female mice to generate SmoA1/+; p27^{Kip1}/+ F1 mice. Intercrossing these mice led to other genotypes used for analysis. SmoA1 mice were genotyped by PCR as previously described.³⁶ To distinguish hemizygous from homozygous SmoA1 mice, QPCR was performed as described in www.jax.org.

CGNP culture. CGNP cultures were generated as previously described.⁴ Cells were plated on individual poly-DL-ornithine (Sigma) pre-coated plates or pre-coated glass coverslips for immunostaining. Where indicated, Shh (R&D Systems) was used at a concentration of 3 µg/mL for 48 hrs.

Immunoblotting, immunoprecipitation and subcellular fractionation. Protein extracts were prepared as previously described.⁵ A total of 50 µg murine cerebella and medulloblastoma protein, were run on 8-12% SDS-polyacrylamide gels and transferred to a PVDF membrane (Millipore). The blots were blocked in 5% milk for one hour at room temperature and incubated with primary antibodies in 3% BSA (in TBS-T) or 5% milk overnight at 4°C. Blots were washed three times and incubated with secondary antibodies in 5% milk in TBS-T for two hours at room temperature. After washing, the signals were developed using the enhanced chemiluminescence method (Amersham), and the membranes were exposed to Kodak Biomax film. Primary antibodies were: total p27 (BD Transduction Labs), phospho-p27 S10 and T187 (Santa Cruz), Cdk4 (C-22; Santa Cruz), Cdk6 (C-21; Santa Cruz), cyclin D1 (H-295; Santa Cruz), cyclin D2 (M-20; Santa Cruz), cyclin E (M-20; Santa Cruz), cyclin A (H-432; Santa Cruz), N-myc (C-19; Santa Cruz), Bmi-1 (Upstate), phospho- and total rp-S6 (Cell Signaling), Src (Cell Signaling), c-Abl (K-12; Santa Cruz) and β-tubulin (Sigma). HRP conjugated secondary antibodies were: goat anti-rabbit IgG (H+L) (Thermo Scientific) and donkey anti-mouse IgG (H+L) (Jackson Immuno Research).

For immunoprecipitation studies, 1 mg of protein extract was used in each case. Ten µg of antibody were incubated with protein A-sepharose for 2 h. Protein extracts were precleared with protein A-sepharose for 2 h and then incubated with the antibody plus protein A-sepharose overnight. The precipitate was washed four times and proteins were eluted with 0.2 M glycine and neutralized with 1M Tris pH 7.4. Antibodies used for immunoprecipitation were same as above. Rabbit IgG was used as control (Upstate Biotechnologies).

Subcellular fractionation was performed using NE-PER Nuclear and Cytoplasmic Extraction Reagents (Pierce) following the manufacturer's instructions. Protein content was determined by using the Bio-Rad protein assay. Antibodies used for subcellular fractionation were: p27 (BD Transduction Labs), RhoA (119; Santa Cruz), GAPDH (Cell Signaling), and c-jun (Calbiochem).

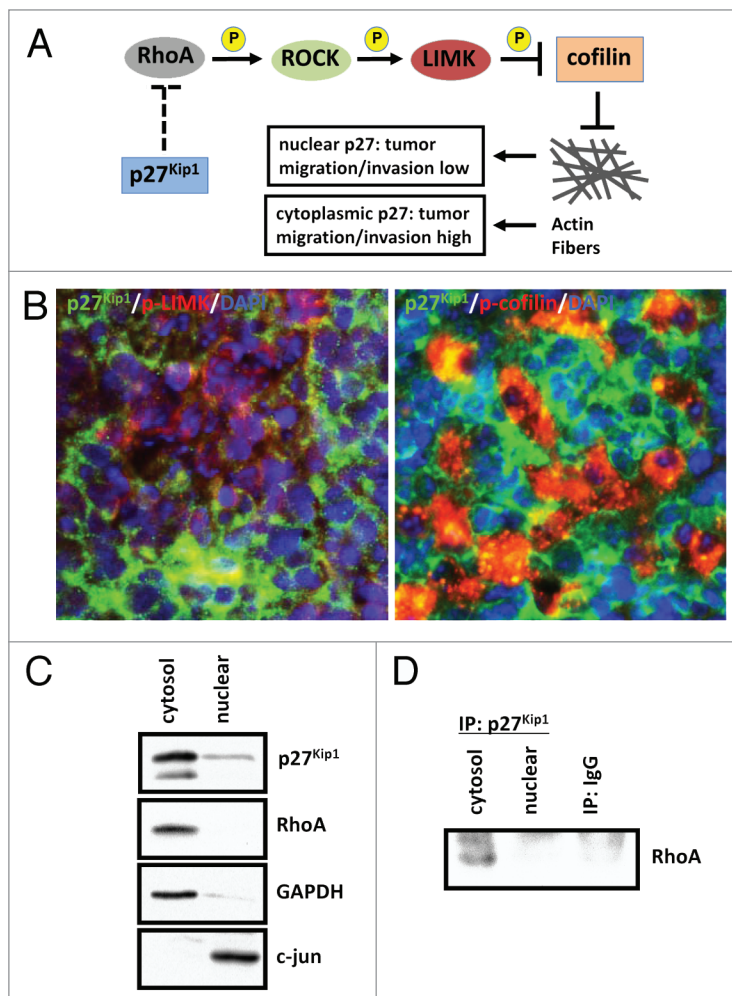


Figure 4. p27^{Kip1} plays a role in cell motility in SmoA1 medulloblastoma. (A) Schematic diagram of p27^{Kip1} regulating cell motility in tumor cells. (B) Immunofluorescence shows p27^{Kip1} is inversely correlated with stabilized cell motility, as evidenced by p27^{Kip1} (green), active phosphorylated-LIMK to prevent cell motility (red, left panel) and inactive phosphorylation of LIMK substrate and actin-depolymerization protein cofilin (red, right panel) in SmoA1 medulloblastoma. (C) Subcellular fractionation of SmoA1 medulloblastoma shows p27^{Kip1} and cell motility regulator RhoA are localized mainly in the cytoplasm. GAPDH serves as cytosolic control and c-jun as nuclear control. (D) Immunoprecipitation of p27^{Kip1} reveals interaction with RhoA. This data suggests p27^{Kip1} is needed to positively regulate cell motility in SmoA1 medulloblastoma.

Immunofluorescence. CGNPs were fixed in 4% PFA for 10 minutes. Cells were then washed with 1xPBS and permeabilized in 1% TritonX-100 for 5 minutes. Cells were blocked in 5% goat serum in PBS-T (1xPBS and 0.1% TritonX-100) for one hour at room temperature, washed once with 1xPBS and then incubated with primary antibody in 2.5% goat serum (in PBS-T) overnight at 4°C. They were washed three times with 1xPBS and incubated with secondary antibody for two hours at room temperature, then washed and mounted in DAPI-containing mounting medium (Vector Labs).

Paraffin-embedded tissue slides were processed as previously described before incubation with primary antibodies.¹¹ Primary antibodies used were: p27 (BD Transduction Labs), PCNA

(Calbiochem), phospho-Histone H3 S10 (Cell Signaling) phospho-LIMK1/2 T508/505 (Santa Cruz) and phospho-cofilin S3 (Cell Signaling). Secondary fluorescent-tagged antibodies were: Alexa Fluor goat anti-rabbit 488/594 (Invitrogen) and Alexa Fluor goat anti-mouse 488/594 (Invitrogen).

Immunostaining performed on cultured cells or tissue sections was visualized using a Leica DM5000B microscope, and images were captured with Leica FW400 software. For quantification of phospho-Histone H3 immunostaining, TIFF images of four random fields were taken for each experimental group using

the 10X objective. The percentage of P-Histone-H3-positive cells over the total number of cells, as determined by DAPI staining, was calculated using Image Pro Plus software (MediaCybernetics).

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